



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 101735, 916
Source: IFWO
Date Processed by STIC: 10-14-04

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

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1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. ~~Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):~~
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IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/735,916

DATE: 10/14/2004

TIME: 11:22:26

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10142004\J735916.raw

4 <110> APPLICANT: GOETSCH, Liliane
 5 CORVAIA, Nathalie
 6 LEGER, Olivier
 7 DUFLOS, Alain
 8 BECK, Alain
 9 HAEUW, Jean-Francois
 11 <120> TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
 13 <130> FILE REFERENCE: 017753-183
 15 <140> CURRENT APPLICATION NUMBER: US 10/735,916
 16 <141> CURRENT FILING DATE: 2003-12-16
 18 <150> PRIOR APPLICATION NUMBER: FR 03/08 538
 19 <151> PRIOR FILING DATE: 2003-07-11
 21 <150> PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
 22 <151> PRIOR FILING DATE: 2003-01-20
 24 <150> PRIOR APPLICATION NUMBER: FR 02/00 653
 25 <151> PRIOR FILING DATE: 2002-01-18
 27 <150> PRIOR APPLICATION NUMBER: FR 02/00 654
 28 <151> PRIOR FILING DATE: 2002-01-18
 30 <150> PRIOR APPLICATION NUMBER: FR 02/05 753
 31 <151> PRIOR FILING DATE: 2002-05-07
 33 <160> NUMBER OF SEQ ID NOS: 156
 35 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

1255 <210> SEQ ID NO: 72
 1256 <211> LENGTH: 117
 1257 <212> TYPE: PRT
 1258 <213> ORGANISM: Homo sapiens
 1260 <400> SEQUENCE: 72
 1261 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1262 1 5 10 15
 1264 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Tyr
 1265 20 25 30
 1267 Trp Ser Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 1268 35 40 45
 E--> 1270 Ile Gly Arg Ile Tyr Tyr Ser Gly Ser Thr Xaa Tyr Asn Pro Ser Leu
 1271 50 55 60
 1273 Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 1274 65 70 75 80
 1276 Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 1277 85 90 95

explanation for
 Xaa is
 mandatory
 see p 6

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1279 Ala Arg Glu Leu Pro Gly Gly Tyr Asp Val Trp Gly Gln Gly Thr Leu
1280              100              105              110
1282 Val Thr Val Ser Ser
1283              115
1423 <210> SEQ ID NO: 77
1424 <211> LENGTH: 135
1425 <212> TYPE: PRT
1426 <213> ORGANISM: Homo sapiens
1428 <400> SEQUENCE: 77
1429 Met Lys Val Leu Ser Leu Leu Tyr Leu Leu Thr Ala Ile Pro Gly Ile
1430   1              5              10              15
1432 Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
1433              20              25              30
1435 Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr
1436              35              40              45
1438 Gly Gly Tyr Leu Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
1439   50              55              60
1441 Glu Trp Met Gly Tyr Ile Ser Tyr Asp Gly Thr Asn Asn Tyr Lys Pro
1442  65              70              75              80
1444 Ser Leu Lys Asp Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln
1445              85              90              95
1447 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
1448              100              105              110
1450 Tyr Cys Ala Arg Tyr Gly Arg Val Phe Phe Asp Tyr Trp Gly Gln Gly
1451              115              120              125
1453 Thr Leu Val Thr Val Ser Ser
1454   130              135
1554 <210> SEQ ID NO: 81
1555 <211> LENGTH: 135
1556 <212> TYPE: PRT
1557 <213> ORGANISM: Homo sapiens
1559 <400> SEQUENCE: 81
1560 Met Lys Val Leu Ser Leu Leu Tyr Leu Leu Thr Ala Ile Pro Gly Ile
1561   1              5              10              15
1563 Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
1564              20              25              30
1566 Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr
1567              35              40              45
1569 Gly Gly Tyr Leu Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
1570   50              55              60
1572 Glu Trp Ile Gly Tyr Ile Ser Tyr Asp Gly Thr Asn Asn Tyr Lys Pro
1573  65              70              75              80
1575 Ser Leu Lys Asp Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln
1576              85              90              95
1578 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
1579              100              105              110
1581 Tyr Cys Ala Arg Tyr Gly Arg Val Phe Phe Asp Tyr Trp Gly Gln Gly
1582              115              120              125
1584 Thr Leu Val Thr Val Ser Ser

```

130 (OK)
↓
shows up
on next
page.

135
—

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```

E--> 1585      130
1635 <210> SEQ ID NO: 84
1636 <211> LENGTH: 445
1637 <212> TYPE: DNA
1638 <213> ORGANISM: Homo sapiens
1640 <220> FEATURE:
1641 <221> NAME/KEY: CDS
1642 <222> LOCATION: (22)..(426)
1644 <400> SEQUENCE: 84
1645 gtcagaacgc gtgccgccac c atg aaa gtg ttg agt ctg ttg tac ctc ttg 51
1646                               Met Lys Val Leu Ser Leu Leu Tyr Leu Leu
1647                               1 5 10
1649 aca gcc att cct ggt atc ctg tct cag gtg cag ctt cag gag tgc ggc 99
1650 Thr Ala Ile Pro Gly Ile Leu Ser Gln Val Gln Leu Gln Glu Ser Gly
1651                               15 20 25
1653 cca gga ctg gtg aag cct tgc gag acc ctg tcc ctc acc tgc act gtc 147
1654 Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val
1655                               30 35 40
1657 tct ggt tac tcc atc agc ggt ggt tat tta tgg aac tgg ata cgg cag 195
E--> 1658 ser gly tyr ser Ile ser gly gly tyr Leu trp asn trp Ile arg gln 45 50 55
E--> 1659
E--> 1661 ccc cca ggg aag gga ctg gag tgg atc ggg tat atc agc tac gac ggt 243
1662 Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Asp Gly
W--> 1663 60 65 70
E--> 1665 acc aat aac tac aaa ccc tcc ctc aag gat cga gtc acc ata tca gtg 291
1666 Thr Asn Asn Tyr Lys Pro Ser Leu Lys Asp Arg Val Thr Ile Ser Val
W--> 1667 75 80 85 90
E--> 1669 gac acg tcc aag aac cag ttc tcc ctg aag ctg agc tct gtg acc gct 339
1670 Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala
W--> 1671 95 100 105
E--> 1673 gcg gac act gca gtg tat tac tgt gcg aga tac ggt agg gtc ttc ttt 387
1674 Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Gly Arg Val Phe Phe
W--> 1675 110 115 120
E--> 1677 gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggtgagtggga 436
1678 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
W--> 1679 125 130
E--> 1681 tcctctgcg 445
1684 <210> SEQ ID NO: 85
1685 <211> LENGTH: 135
1686 <212> TYPE: PRT
1687 <213> ORGANISM: Homo sapiens
1689 <400> SEQUENCE: 85
1690 Met Lys Val Leu Ser Leu Leu Tyr Leu Leu Thr Ala Ile Pro Gly Ile
1691 1 5 10 15
1693 Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
1694 20 25 30
1696 Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser
1697 35 40 45
1699 Gly Gly Tyr Leu Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu

```


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```
1700      50      55      60
1702 Glu Trp Ile Gly Tyr Ile Ser Tyr Asp Gly Thr Asn Asn Tyr Lys Pro
1703 65      70      75      80
1705 Ser Leu Lys Asp Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
1706      85      90      95
1708 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
1709      100      105      110
1711 Tyr Cys Ala Arg Tyr Gly Arg Val Phe Phe Asp Tyr Trp Gly Gln Gly
1712      115      120      125
1714 Thr Leu Val Thr Val Ser Ser
E--> 1715      130
```

135

VARIABLE LOCATION SUMMARY

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Output Set: N:\CRF4\10142004\J735916.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:60; Xaa Pos. 35,36,39,99

Seq#:72; Xaa Pos. 59

Seq#:84; N Pos. 219,226

VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

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L:897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:32
M:341 Repeated in SeqNo=60
L:1270 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:72
L:1418 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:76
L:1454 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:77
L:1549 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:80
L:1585 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:81
L:1658 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:84
L:1658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:195
L:1658 M:254 E: No. of Bases conflict, LENGTH:Input:45 Counted:243 SEQ:84
L:1658 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:1658 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=84
L:1663 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:84
L:1667 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:84
L:1671 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:84
L:1675 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:84
L:1679 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:84
L:1681 M:252 E: No. of Seq. differs, <211> LENGTH:Input:445 Found:493 SEQ:84
L:1715 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:85